

Basic Local Alignment Search Tool

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Blast 2 sequences

dbj|BB611382.1| (591 letters)

Results for:

dbj|BB611382.1 BB611382 RIKEN full-length enriched, adult male hippocampus Mus musculus cDNA clone 2900055L15 5' (591bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|16452632|dbj|BB611382.1|

gi|16452632|dbj|BB611382.1|

Description

BB611382 RIKEN full-length enriched, adult male hippocampus Mus musculus cDNA clone 2900055L15 5'.

Molecule type

rna

Query Length

591

Subject ID

31643

Description

None

Molecule type

nucleic acid

Subject Length

2208

Program

BLASTN 2.2.24+ [Citation](#)

Reference

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Other reports: [Search Summary](#) [Taxonomy reports](#)

[Search Parameters](#)

Search parameter name Search parameter value

Program	blastn
Word size	28
Expect value	10
Hittlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

Results Statistics

Results Statistics parameter name Results Statistics parameter value

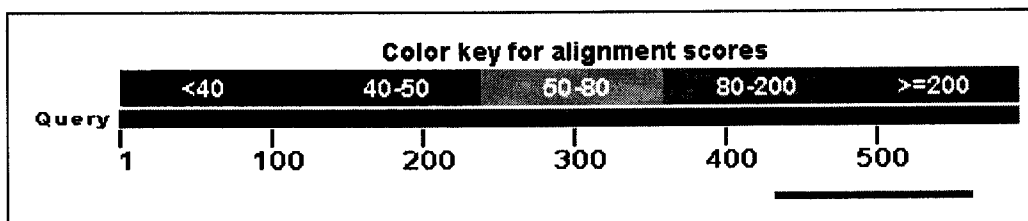
Effective search space	1268710
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Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Plot of gi|16452632|dbj|BB611382.1| vs 31643 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



Descriptions

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map Viewer **P** PubChem BioAssay
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
31643		202	202	21%	1e-55	94%	

Alignments

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)

```
>lcl|31643
Length=2208
```

```
Score = 202 bits (109), Expect = 1e-55
Identities = 123/130 (95%), Gaps = 0/130 (0%)
Strand=Plus/Plus
```

```
Query  432  ATGCATTGTGGGTTACTGGAGGAACCCGACATGGATTCCACAGAGAGCTGGATTGAAAGA  491
      |||
Sbjct   1    ATGCATTGTGGGTTACTGGAGGAACCCGACATGGATTCCACAGAGAGCTGGATTGAAAGA  60

Query  492  TGTCTCAATGAAAGCGAGAATAAACGCTATTCCAGTCACACATCTCTGGGGAATGTGTCT  551
      |||
Sbjct   61  TGTCTCAACGAAAGTGAACAAACGTTATTCCAGCCACACATCTCTGGGGAATGTTTCT  120

Query  552  AATGATGAAA  561
      |||
Sbjct  121  AATGATGAAA  130
```

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)